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LETTER

INFECTIOUS DISEASE

Estimation of basic reproduction number for COVID-19 and the reasons for its differences

To the Editor,

The novel coronavirus pneumonia is an acute respiratory disease. In December 2019, this disease emerged in Wuhan, China. The Chinese government called it SARS-CoV-2 which was subsequently named COVID-19 by the World Health Organization (WHO).[1] In January 2020, WHO confirmed it as a sustained human to human disease.[2] By March 2020, COVID-19 had been transmitted round the world rapidly and everyday large number of new cases were registered. COVID-19 is a leaped type of coronavirus family, such as severe acute respiratory syndrome (SARS) and the Middle East respiratory syndrome (MERS), that has been transmitted from wild animals to human.[3]

Since COVID-19 has become a global concern, much research has been done to control its transmission. Basic reproduction number (R_0) is one of the most widely used concept in epidemiology for understanding the contagiousness of an infectious agent. R_0 is the average number of new infections produced by an infectious patient in a given population. This concept, which is calculated as a numerical index, is used when there is a dynamic infectious disease and the population is not vaccinated.[4] There are three values for this index followed by three interpretations: if it is greater than one, the contagion is expected to continue. If smaller than one, it means that the contagion is running out and if equal to one it implies that almost the stability conditions are dominated.[5] Hence, R_0 can represent a potential measure of the contagion of a contagious disease. The present study gives a brief discussion on key aspects of the concept of R_0 and its significance to the coronavirus pandemic.

As at March 2020, several studies have calculated R_0 in different populations for COVID-19. Most of these studies are from China and cover the first 2 months of 2020. Investigation on these studies revealed that the minimum R_0 for China and overseas was 1.4 while the maximum was 7.23. For Italy, it was estimated as 4.2. Moreover, these values were larger compared to SARS and MERS. Therefore, COVID-19 can be considered as a high transmission disease with respect to SARS and MERS. The method of calculation in these studies included mathematical, statistical or stochastic methods. A review article by Liu et al, which investigated some of these studies, shows that in articles using the stochastic method, the mean R_0 is 2.44 and in the mathematical methods the mean is 4.2 and for studies which used the statistical method is 2.6.[6] Comparison of these numbers shows that the mathematical method had larger values compared with other methods. Moreover, the estimated R_0 values were larger than that of the WHO (range 1.4-2.5).

R_0 is a biological fact which is calculated using complex mathematical models and with a set of assumptions about the population under study. Therefore, the interpretation of these models needs an understanding of the initial model and its inputs. Usually, three parameters—(a) the duration of contagiousness after a person becomes infected, (b) the likelihood of infection per contact between a susceptible person and an infectious person or vector and (c) the contact rate—are used in the construction of the R_0, each of them may differ in the population under study. Epidemiological factors such as environmental conditions, agent hosts, governments' policies on environmental control and access to public health resources also can in turn change in mentioned parameters.[7] Another factor which can change the model's parameters is the contact rate, while factors such as population density, social organisation and seasonality may cause variation in contact rate. On the other hand, many model parameters are dependent on the available data, and here the quality of the data is definitely important. In critical situations such as the contagion of COVID-19, it may be difficult to collect accurate and definitive data. However, some studies have used data-driven methods to estimate R_0 in COVID-19. Therefore, when estimating a value for R_0 at a given place and time, using different models which differ slightly in initial assumptions could lead to different estimates.[8]

One of the most effective strategies of controlling the spread of contagious infections is quarantine. It prevents infected people from contacting the susceptible population. Another is isolation, in which the sick person is separated from healthy people. These strategies have shown beneficial effects in similar diseases and can also be effective in reducing R_0 of COVID-19. Differences in R_0 estimates can be a controversial issue, but are not reasons for R_0 inefficiency. R_0 index may differ by time, hence its value should be coordinated by time.

In conclusion, R_0 is a very useful index when making decisions to control infectious diseases including COVID-19, considering its specific population structure. However, in using the initial assumption for any model, precaution is needed.

DISCLOSURE

None.

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